RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/534,043_

Source: _PCT_

Date Processed by STIC: _6/20/06_

ENTERED

PCT

```
 3 <110> APPLICANT: SAKAGUCHI, Nobuo
 5 <120> TITLE OF INVENTION: TRANSGENIC MAMMAL CARRYING GANP GENE TRANSFERRED THEREINTO
AND
 6       UTILIZATION THEREOF
 8 <130> FILE REFERENCE: 4456-0104PUS1
10 <140> CURRENT APPLICATION NUMBER: US 10/534,043
11 <141> CURRENT FILING DATE: 2005-05-05
13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/014221
14 <151> PRIOR FILING DATE: 2003-11-07
16 <150> PRIOR APPLICATION NUMBER: PCT/JP02/11598
17 <151> PRIOR FILING DATE: 2002-11-07
19 <160> NUMBER OF SEQ ID NOS: 105
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 6429
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (384)..(6299)
33 <400> SEQUENCE: 1
34 gttgcggtgc ggtgggcccg gtagaggctg cacgcagact gtgggcgagc acaagcgctg      60
36 gcgacagtgg ccgtatctgg cggacttgct cctccctccg cggcctccgc tgtcccttgt     120
38 gtctttgccg agttgctgaa ggccttcact agtcttcgct cgaaggcgtc tgttaaccta     180
40 gcggccggct tccggagtgt taagcatcgg ggataaaaag ctattatttc tagaccaggg     240
42 catcgcaagt tcgagttacc gggagaaaaa tgagatggtc atcctgagga tgaaggagag     300
44 cttcccctgg caacagataa tttaaagagg agagctactt gtgtatagtc catatttatt     360
46 gccttcagat aattggcttg aag atg cac ccg gtg aac ccc ttc gga ggc agc     413
47                          Met His Pro Val Asn Pro Phe Gly Gly Ser
48                           1               5                   10
50 agc cca agt gct ttt gcg gta tct tcc agc acc acg gga aca tat cag     461
51 Ser Pro Ser Ala Phe Ala Val Ser Ser Ser Thr Thr Gly Thr Tyr Gln
52               15              20                  25
54 act aaa tca cca ttt cga ttt ggc cag cct tcc ctt ttt gga cag aac     509
55 Thr Lys Ser Pro Phe Arg Phe Gly Gln Pro Ser Leu Phe Gly Gln Asn
56           30              35                  40
58 agc aca ccc agc aag agc ctg gcg ttt tca caa gta cca agc ttt gca     557
59 Ser Thr Pro Ser Lys Ser Leu Ala Phe Ser Gln Val Pro Ser Phe Ala
60           45              50                  55
62 aca ccc tct gga gga agc cat tct tcc tcc ttg cca gca ttt gga ctc     605
63 Thr Pro Ser Gly Gly Ser His Ser Ser Ser Leu Pro Ala Phe Gly Leu
64     60              65                  70
66 acc caa acc tca agt gtg gga ctc ttc tct agt ctc gaa tcc aca cct     653
67 Thr Gln Thr Ser Ser Val Gly Leu Phe Ser Ser Leu Glu Ser Thr Pro
```

```
68 75                    80                   85                   90
70 tct ttc gca gct act tcg agt tcc tct gtg ccc ggc aat acg gca ttc      701
71 Ser Phe Ala Ala Thr Ser Ser Ser Ser Val Pro Gly Asn Thr Ala Phe
72                   95                  100                  105
74 agc ttt aag tca acc tct agc gtt ggg gtt ttc cca agt ggc gct act      749
75 Ser Phe Lys Ser Thr Ser Ser Val Gly Val Phe Pro Ser Gly Ala Thr
76              110                  115                  120
78 ttt ggg cca gaa acc gga gaa gta gca ggt tct ggc ttt cgg aag acg      797
79 Phe Gly Pro Glu Thr Gly Glu Val Ala Gly Ser Gly Phe Arg Lys Thr
80              125                  130                  135
82 gaa ttc aag ttt aaa cct ctg gaa aat gca gtc ttc aaa ccg ata ccg      845
83 Glu Phe Lys Phe Lys Pro Leu Glu Asn Ala Val Phe Lys Pro Ile Pro
84        140                  145                  150
86 ggg cct gag tca gag cca gaa aaa acc cag agc cag att tct tct gga      893
87 Gly Pro Glu Ser Glu Pro Glu Lys Thr Gln Ser Gln Ile Ser Ser Gly
88 155                  160                  165                  170
90 ttt ttt aca ttt tcc cat ccc gtt ggt agc ggg tct gga ggc ctg acc      941
91 Phe Phe Thr Phe Ser His Pro Val Gly Ser Gly Ser Gly Gly Leu Thr
92        .            175                  180                  185
94 cct ttt tct ttc cca cag gtg aca aat agt tcg gtg act agc tca agt      989
95 Pro Phe Ser Phe Pro Gln Val Thr Asn Ser Ser Val Thr Ser Ser Ser
96              190                  195                  200
98 ttt atc ttt tcg aaa cca gtt act agt aat act cct gcc ttt gcc tct     1037
99 Phe Ile Phe Ser Lys Pro Val Thr Ser Asn Thr Pro Ala Phe Ala Ser
100           205                  210                  215
102 cct ttg tct aac caa aat gta gaa gaa gag aag agg gtt tct acg tca     1085
103 Pro Leu Ser Asn Gln Asn Val Glu Glu Glu Lys Arg Val Ser Thr Ser
104           220                  225                  230
106 gcg ttt gga agc tca aac agt agc ttc agt act ttc ccc aca gcg tca     1133
107 Ala Phe Gly Ser Ser Asn Ser Ser Phe Ser Thr Phe Pro Thr Ala Ser
108 235                  240                  245                  250
110 cca gga tct ttg ggg gag ccc ttc cca gct aac aaa cca agc ctc cgc     1181
111 Pro Gly Ser Leu Gly Glu Pro Phe Pro Ala Asn Lys Pro Ser Leu Arg
112              255                  260                  265
114 caa gga tgt gag gaa gcc atc tcc cag gtg gag cca ctt ccc acc ctc     1229
115 Gln Gly Cys Glu Glu Ala Ile Ser Gln Val Glu Pro Leu Pro Thr Leu
116           270                  275                  280
118 atg aag gga tta aag agg aaa gag gac cag gat cgc tcc ccg agg aga     1277
119 Met Lys Gly Leu Lys Arg Lys Glu Asp Gln Asp Arg Ser Pro Arg Arg
120           285                  290                  295
122 cat tgc cac gag gca gca gaa gac cct gat ccc ctg tcc agg ggc gac     1325
123 His Cys His Glu Ala Ala Glu Asp Pro Asp Pro Leu Ser Arg Gly Asp
124        300                  305                  310
126 cat ccc cca gat aaa cgg cca gtc cgc ctc aac aga ccc cgg gga ggt     1373
127 His Pro Pro Asp Lys Arg Pro Val Arg Leu Asn Arg Pro Arg Gly Gly
128 315                  320                  325                  330
130 act ttg ttt ggc cgg aca ata cag gag gtc ttc aaa agc aat aaa gag     1421
131 Thr Leu Phe Gly Arg Thr Ile Gln Glu Val Phe Lys Ser Asn Lys Glu
132              335                  340                  345
```

```
134 gca ggc cgc ctg ggc agc aag gaa tcc aag gag agt ggc ttt gcg gaa    1469
135 Ala Gly Arg Leu Gly Ser Lys Glu Ser Lys Glu Ser Gly Phe Ala Glu
136         350             355             360
138 cct ggg gaa agt gac cac gcg gcc gtc cca gga ggg agt cag tcc acc    1517
139 Pro Gly Glu Ser Asp His Ala Ala Val Pro Gly Gly Ser Gln Ser Thr
140         365             370             375
142 atg gta cct tcc cgc ctt cca gct gtg act aaa gag gaa gaa gaa agt    1565
143 Met Val Pro Ser Arg Leu Pro Ala Val Thr Lys Glu Glu Glu Glu Ser
144     380             385             390
146 aga gat gag aaa gaa gat tct ctc agg gga aag tct gtg cgc cag agt    1613
147 Arg Asp Glu Lys Glu Asp Ser Leu Arg Gly Lys Ser Val Arg Gln Ser
148 395             400             405                 410
150 aag cga agg gaa gag tgg atc tac agc ctc ggg ggc gtg tct tct tta    1661
151 Lys Arg Arg Glu Glu Trp Ile Tyr Ser Leu Gly Gly Val Ser Ser Leu
152             415             420             425
154 gag ctc aca gcc atc cag tgc aag aac atc ccc gac tac ctc aac gac    1709
155 Glu Leu Thr Ala Ile Gln Cys Lys Asn Ile Pro Asp Tyr Leu Asn Asp
156         430             435             440
158 aga gcc atc ctg gag aaa cac ttc agc aaa atc gct aaa gtc cag cgg    1757
159 Arg Ala Ile Leu Glu Lys His Phe Ser Lys Ile Ala Lys Val Gln Arg
160     445             450             455
162 gtc ttc acc aga cgc agc aag aag ctc gcc gtg att cat ttt ttc gac    1805
163 Val Phe Thr Arg Arg Ser Lys Lys Leu Ala Val Ile His Phe Phe Asp
164     460             465             470
166 cac gca tcg gca gcc ctg gct agg aag aag ggg aaa ggt ctg cat aag    1853
167 His Ala Ser Ala Ala Leu Ala Arg Lys Lys Gly Lys Gly Leu His Lys
168 475             480             485                 490
170 gac gtg gtt atc ttt tgg cac aag aag aaa ata agt ccc agc aag aaa    1901
171 Asp Val Val Ile Phe Trp His Lys Lys Lys Ile Ser Pro Ser Lys Lys
172             495             500             505
174 ctc ttt ccc ctg aag gag aag ctt ggt gag agt gaa gcc agc cag ggc    1949
175 Leu Phe Pro Leu Lys Glu Lys Leu Gly Glu Ser Glu Ala Ser Gln Gly
176         510             515             520
178 atc gag gac tcc ccc ttt cag cac tcg cct ctc agc aag ccc atc gtg    1997
179 Ile Glu Asp Ser Pro Phe Gln His Ser Pro Leu Ser Lys Pro Ile Val
180     525             530             535
182 agg cct gca gcc ggc agc ctc ctc agc aaa agc tct cca gtg aag aag    2045
183 Arg Pro Ala Ala Gly Ser Leu Leu Ser Lys Ser Ser Pro Val Lys Lys
184     540             545             550
186 ccg agt ctt ctg aag atg cac cag ttt gag gcg gat cct ttt gac tct    2093
187 Pro Ser Leu Leu Lys Met His Gln Phe Glu Ala Asp Pro Phe Asp Ser
188 555             560             565                 570
190 gga tct gag ggc tcc gag ggc ctt ggt tct tgc gtg tca tct ctt agc    2141
191 Gly Ser Glu Gly Ser Glu Gly Leu Gly Ser Cys Val Ser Ser Leu Ser
192             575             580             585
194 acc ctg ata ggg act gtg gca gac aca tct gag gag aag tac cgc ctt    2189
195 Thr Leu Ile Gly Thr Val Ala Asp Thr Ser Glu Glu Lys Tyr Arg Leu
196         590             595             600
198 ctg gac cag aga gac cgc atc atg cgg caa gct cga gtg aag agg acg    2237
```

```
199 Leu Asp Gln Arg Asp Arg Ile Met Arg Gln Ala Arg Val Lys Arg Thr
200         605             610             615
202 gac ctg gac aaa gcc agg gca ttt gtt ggg act tgc cct gac atg tgt    2285
203 Asp Leu Asp Lys Ala Arg Ala Phe Val Gly Thr Cys Pro Asp Met Cys
204     620             625             630
206 ccc gag aag gag cgg tac ttg agg gag acc cgg agc cag ctg agc gtg    2333
207 Pro Glu Lys Glu Arg Tyr Leu Arg Glu Thr Arg Ser Gln Leu Ser Val
208 635             640             645             650
210 ttt gaa gtt gtc cca ggg act gac cag gtg gac cat gca gca gcc gtg    2381
211 Phe Glu Val Val Pro Gly Thr Asp Gln Val Asp His Ala Ala Ala Val
212             655             660             665
214 aag gag tac agc cgg tcc tct gca gat cag gag gag ccc ctg cca cat    2429
215 Lys Glu Tyr Ser Arg Ser Ser Ala Asp Gln Glu Glu Pro Leu Pro His
216         670             675             680
218 gag ctg aga ccc tca gca gtt ctc agc agg acc atg gac tac ctg gtg    2477
219 Glu Leu Arg Pro Ser Ala Val Leu Ser Arg Thr Met Asp Tyr Leu Val
220         685             690             695
222 acc cag atc atg gac caa aag gaa ggc agc ctt cgg gat tgg tat gac    2525
223 Thr Gln Ile Met Asp Gln Lys Glu Gly Ser Leu Arg Asp Trp Tyr Asp
224     700             705             710
226 ttc gtg tgg aac cgc acc cgg ggt ata cgg aag gac ata aca cag cag    2573
227 Phe Val Trp Asn Arg Thr Arg Gly Ile Arg Lys Asp Ile Thr Gln Gln
228 715             720             725             730
230 cac ctc tgt gat ccc ctg acg gtg tct ctg atc gag aag tgt acc cga    2621
231 His Leu Cys Asp Pro Leu Thr Val Ser Leu Ile Glu Lys Cys Thr Arg
232             735             740             745
234 ttt cac att cac tgt gcc cac ttt atg tgt gag gag cct atg tct tcc    2669
235 Phe His Ile His Cys Ala His Phe Met Cys Glu Glu Pro Met Ser Ser
236             750             755             760
238 ttt gat gcc aag atc aac aat gag aac atg acc aag tgt cta cag agt    2717
239 Phe Asp Ala Lys Ile Asn Asn Glu Asn Met Thr Lys Cys Leu Gln Ser
240         765             770             775
242 ctg aag gag atg tac cag gac ctg agg aac aag ggt gtt ttt tgt gcc    2765
243 Leu Lys Glu Met Tyr Gln Asp Leu Arg Asn Lys Gly Val Phe Cys Ala
244     780             785             790
246 agt gaa gca gag ttt cag ggc tac aat gtc ctg ctt aat ctc aac aaa    2813
247 Ser Glu Ala Glu Phe Gln Gly Tyr Asn Val Leu Leu Asn Leu Asn Lys
248 795             800             805             810
250 gga gac att ttg aga gaa gtg cag cag ttc cac cct gac gtt agg aac    2861
251 Gly Asp Ile Leu Arg Glu Val Gln Gln Phe His Pro Asp Val Arg Asn
252             815             820             825
254 tcc cca gag gtg aac ttc gct gtc cag gct ttt gct gca ttg aac agc    2909
255 Ser Pro Glu Val Asn Phe Ala Val Gln Ala Phe Ala Ala Leu Asn Ser
256             830             835             840
258 aat aat ttt gtg aga ttt ttc aaa ctg gtt cag tca gct tct tac ctg    2957
259 Asn Asn Phe Val Arg Phe Phe Lys Leu Val Gln Ser Ala Ser Tyr Leu
260         845             850             855
262 aat gcg tgc ctg tta cac tgt tac ttt aat cag atc cgc aag gat gcc    3005
263 Asn Ala Cys Leu Leu His Cys Tyr Phe Asn Gln Ile Arg Lys Asp Ala
```

```
264      860                   865                   870
266 ctc cgg gca ctc aat gtt gct tat act gta agc aca cag cgc tct acc      3053
267 Leu Arg Ala Leu Asn Val Ala Tyr Thr Val Ser Thr Gln Arg Ser Thr
268 875                   880                   885                   890
270 gtc ttc ccc ctg gat ggt gtc gtc cgc atg ctg ctg ttc aga gat agt      3101
271 Val Phe Pro Leu Asp Gly Val Val Arg Met Leu Leu Phe Arg Asp Ser
272              895                   900                   905
274 gaa gag gcg aca aac ttc ctc aat tac cat ggc ctc act gta gct gat      3149
275 Glu Glu Ala Thr Asn Phe Leu Asn Tyr His Gly Leu Thr Val Ala Asp
276              910                   915                   920
278 ggc tgt gtt gag ctg aat cgg tcg gca ttc ttg gaa ccg gag gga tta      3197
279 Gly Cys Val Glu Leu Asn Arg Ser Ala Phe Leu Glu Pro Glu Gly Leu
280          925                   930                   935
282 tgc aag gcc agg aag tca gtg ttt att ggc cgg aag ctg acg gtg tca      3245
283 Cys Lys Ala Arg Lys Ser Val Phe Ile Gly Arg Lys Leu Thr Val Ser
284      940                   945                   950
286 gtt ggg gaa gtt gtg aat gga ggg ccg ttg ccc cct gtt cct cgc cat      3293
287 Val Gly Glu Val Val Asn Gly Gly Pro Leu Pro Pro Val Pro Arg His
288 955                   960                 · 965                   970
290 aca cct gtg tgc agc ttc aac tcc cag aat aag tac gtt gga gag agc      3341
291 Thr Pro Val Cys Ser Phe Asn Ser Gln Asn Lys Tyr Val Gly Glu Ser
292              975                   980                   985
294 ctg gct acg gag ctg ccc atc agc act cag aga gct ggt gga  gac cca      3389
295 Leu Ala Thr Glu Leu Pro Ile Ser Thr Gln Arg Ala Gly Gly  Asp Pro
296              990                   995                   1000
298 gca ggt ggt  ggc aga gga gag gac  tgt gag gca gag gtg  gac ttg      3434
299 Ala Gly Gly  Gly Arg Gly Glu Asp  Cys Glu Ala Glu Val  Asp Leu
300          1005                  1010                  1015
302 cca aca ttg  gcg gtc ctc cca cag  ccg cct cct gca tcc  tca gcc      3479
303 Pro Thr Leu  Ala Val Leu Pro Gln  Pro Pro Pro Ala Ser  Ser Ala
304          1020                  1025                  1030
306 acg ccg gcg  ctt cat gtc cag cca  ctg gcc cca gcc gca  gca ccc      3524
307 Thr Pro Ala  Leu His Val Gln Pro  Leu Ala Pro Ala Ala  Ala Pro
308          1035                  1040                  1045
310 agc ctt ctc  cag gcc tcc acg cag  cct gag gtg ctg ctt  cca aag      3569
311 Ser Leu Leu  Gln Ala Ser Thr Gln  Pro Glu Val Leu Leu  Pro Lys
312          1050                  1055                  1060
314 cct gcg cct  gtg tac tct gac tcg  gac ctg gta cag gtg  gtg gac      3614
315 Pro Ala Pro  Val Tyr Ser Asp Ser  Asp Leu Val Gln Val  Val Asp
316          1065                  1070                  1075
318 gag ctc atc  cag gag gct ctg caa  gtg gac tgt gag gaa  gtc agc      3659
319 Glu Leu Ile  Gln Glu Ala Leu Gln  Val Asp Cys Glu Glu  Val Ser
320          1080                  1085                  1090
322 tcc gct ggg  gca gcc tac gta gcc  gca gct ctg ggc gtt  tcc aat      3704
323 Ser Ala Gly  Ala Ala Tyr Val Ala  Ala Ala Leu Gly Val  Ser Asn
324          1095                  1100                  1105
326 gct gct gtg  gag gat ctg att act  gct gcg acc·acg ggc  att ctg      3749
327 Ala Ala Val  Glu Asp Leu Ile Thr  Ala Ala Thr Thr Gly  Ile Leu
328          1110                  1115                  1120
```

```
L:2633 M:283 W: Missing Blank Line separator, <400> field identifier
L:3042 M:283 W: Missing Blank Line separator, <220> field identifier
L:3152 M:283 W: Missing Blank Line separator, <220> field identifier
```